

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2002, 11:59:46 : Search time 14.07 Seconds
(without alignments)
3.963 Million cell updates/sec

Title: us-08-971-172a-7

Perfect score: 4956

Sequence: 1 ATGAATGGAACATGTTCC.....TAGAGAACTGAAGCTGA 4956

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 5654 residues

number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : turner172.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4855.6	98.0	5654	1 ROBO1_1997	Entered [sdavid 2
c 2	22.4	0.5	5654	1 ROBO1_1997	Entered [sdavid 2

ALIGNMENTS

Result 1
Entered [sdavid 20-Sep-02 10:27]

Query Match 98.0%; Score 4855.6; DB 1; Length 5654;

Best local Similarity 100.0%; Pred. No. 0;

Matches 4855; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGAATGGAACATGTTCCCTTTTGGTCATGATATCACTCTCCAGCTTATCCCAAT	60
DB	510	ATGAATGGAACATGTTCCCTTTTGGTCATGATATCACTCTCCAGCTTATCCCAAT	569
QY	61	CACCTGTTTGGCCAGCTTATTCAGACCTGAAGATAGAGAGGGGAAGACAC	120
DB	570	CACCTGTTTGGCCAGCTTATTCAGACCTGAAGATAGAGAGGGGAAGACAC	629
QY	121	GGAGCGCAATCCCACTCTGATTAACGATGACATTTGCTGGGCTATACAGCTCCGT	180
DB	630	GGAGCGCAATCCCACTCTGATTAACGATGACATTTGCTGGGCTATACAGCTCCGT	689
QY	181	CTTCGTCAGGAAGATTTCACCTCGATGTTGAACACCTTCAGACCTGATTGTCTCA	240
DB	690	CTTCGTCAGGAAGATTTCACCTCGATGTTGAACACCTTCAGACCTGATTGTCTCA	749
QY	241	AAAGGAGAACCTGCAACTTTGAAGTGCMAAGCTGAAGCGCCGCCACACCCACTATTGAA	300
DB		AA	

DB	750	AAAGGAGAACCTGCAACTTTGAAGTGCMAAGCTGAAGCGCCGCCACACCCACTATTGAA	809
QY	301	TGCTACAAAGGGGAGAGAGATGAGACAGACAAAGATACCTCTCCCTACACCCAGT	360
DB	810	TGGTACAAAGGGGAGAGAGATGAGACAGACAAAGATACCTCTCCCTACACCCAGT	869
QY	361	TTGCTGCCAGTGGATCTTATTTTCTTACGATATAGATGAGAGGAAAGATAGACT	420
DB	870	TTGCTGCCAGTGGATCTTATTTTCTTACGATATAGATGAGAGGAAAGATAGACT	929
QY	421	GATGAAGAGCTATATGCTGTGAGCAAGAAATTAACCTTGGAGAGCTGTGACCCAAAT	480
DB	930	GATGAAGAGCTATATGCTGTGAGCAAGAAATTAACCTTGGAGAGCTGTGACCCAAAT	989
QY	481	GCATCGCTGGAAGTAGCCATCTTCGGGATGACTTCAGACAAAACCTTGGATGTATG	540
DB	990	GCATCGCTGGAAGTAGCCATCTTCGGGATGACTTCAGACAAAACCTTGGATGTATG	1049
QY	541	GTTGCAGTAGAGAGCTGAGTAAATGGAATGCCAATCTCCAGAGGCCATCTGAGCC	600
DB	1050	GTTGCAGTAGAGAGCTGAGTAAATGGAATGCCAATCTCCAGAGGCCATCTGAGCC	1109
QY	601	ACCATTTTCATGAAGAAGATGCTCTCCACTGGATGATTAAGATGAAGAATTAATATA	660
DB	1110	ACCATTTTCATGAAGAAGATGCTCTCCACTGGATGATTAAGATGAAGAATTAATATA	1169
QY	661	CGAGGAGAAAGCTCATGATCACTTACACCCGTAAGAAAGTACGCTGCAAAATATGTTGT	720
DB	1170	CGAGGAGAAAGCTCATGATCACTTACACCCGTAAGAAAGTACGCTGCAAAATATGTTGT	1229
QY	721	GTTGGTACCAATATGTTGGGGAACGTGAGAGTGAAGTACCGGAGCTGACTGCTTATG	780
DB	1230	GTTGGTACCAATATGTTGGGGAACGTGAGAGTGAAGTACCGGAGCTGACTGCTTATG	1289
QY	781	AGACCATCATTTGTAAGAGAGACCCAGTAACCTTGGCACTAGTGATGACAGTGCAGAA	840
DB	1290	AGACCATCATTTGTAAGAGAGACCCAGTAACCTTGGCACTAGTGATGACAGTGCAGAA	1349
QY	841	TTTAAATGTAGAGCCGAGGTGACCTGTACCTACAGTACGATGAGAGAAAGATGATGA	900
DB	1350	TTTAAATGTAGAGCCGAGGTGACCTGTACCTACAGTACGATGAGAGAAAGATGATGA	1409
QY	901	GAGCTGCCCAATCCATATGTAAGAAATCCGAGATGATACCTTGAATAATTAGAAAGTG	960
DB	1410	GAGCTGCCCAATCCATATGTAAGAAATCCGAGATGATACCTTGAATAATTAGAAAGTG	1469
QY	961	ACAAGCTGATGATGAGTTCATACACTTGTGTCAGAGAAATATGTTGGCCAAAGCTGAA	1020
DB	1470	ACAAGCTGATGATGAGTTCATACACTTGTGTCAGAGAAATATGTTGGCCAAAGCTGAA	1529
QY	1021	GCATCTGCTACTGATGCTGTTCAAGAACCTCCACATTTTGTGTGAACCCCGTGACAG	1080
DB	1530	GCATCTGCTACTGATGCTGTTCAAGAACCTCCACATTTTGTGTGAACCCCGTGACAG	1589
QY	1081	GTTGTTGCTTTGGAGCGAGCTGTAACCTTTCAGTGTGAACACCGGAATTCCTCAACA	1140
DB	1590	GTTGTTGCTTTGGAGCGAGCTGTAACCTTTCAGTGTGAACACCGGAATTCCTCAACA	1649
QY	1141	GCTATTTTCTGAGAGAGAGAGGAGTCAAGATCTTCTTCATATTCACACCAACAG	1200
DB	1650	GCTATTTTCTGAGAGAGAGAGGAGTCAAGATCTTCTTCATATTCACACCAACAG	1709
QY	1201	TCATCCAGCCGATTTTATAGTCTCCAGACATGCGGACCTCACAATTAATATGTCACGGA	1260
DB	1710	TCATCCAGCCGATTTTATAGTCTCCAGACATGCGGACCTCACAATTAATATGTCACGGA	1769
QY	1261	TCGATGTTGTTATTCATCTGCAAGATTTAAATGTCTGGAACATCATCACAAAG	1320
DB	1770	TCGATGTTGTTATTCATCTGCAAGATTTAAATGTCTGGAACATCATCACAAAG	1829
QY	1321	GCAATATTGGAAGTTACAGATGTGATGTCAGATGCGCTCCCACTTATTCGACAAAGT	1380
DB	1830	GCAATATTGGAAGTTACAGATGTGATGTCAGATGCGCTCCCACTTATTCGACAAAGT	1889

Oy 1381 CCTGGAATCAGACGTGTAGCCGCTGGAGTGGCACTTTCCTCAGTGTGTGGCCACAGGC 1440
 |||||
 Db 1890 CCTGTGAATCAACACTGTAGCCCTGGATGGCACTTTCCTCAGCTGTGTGGCCACAGGC 1949
 Oy 1441 ACTCCAGTCCCAACCACTTCTGTGGAGAAAGATGGAGTCTCTGTTTCAACCCAGACTCT 1500
 |||||
 Db 1950 AGTCCAGTCCCAACCACTTCTGTGGAGAAAGATGGAGTCTCTGTTTCAACCCAGACTCT 2009
 Oy 1501 CGAATCAACAGTGTGGAGAAATGGAGTACTGAGATCCGATGTGCTAAGTGGGTGTACT 1560
 |||||
 Db 2010 CGAATCAACAGTGTGGAGAAATGGAGTACTGAGATCCGATGTGCTAAGTGGGTGTACT 2069
 Oy 1561 GGTGGTACACCTGATGATGATCAACCCCAAGTGTGTAAGCAACATGAGTGTCTACTT 1620
 |||||
 Db 2070 GGTGGTACACCTGATGATGATCAACCCCAAGTGTGTAAGCAACATGAGTGTCTACTT 2129
 Oy 1621 GAAGTTCAGAAATTTGGAGTTCAGATTCAGCTTCCAAAGACTCTCAACCCAAATTTAATC 1680
 |||||
 Db 2130 GAAGTTCAGAAATTTGGAGTTCAGATTCAGCTTCCAAAGACTCTCAACCCAAATTTAATC 2189
 Oy 1681 CCTAGTGGCCCATCAAAACCTGAAGTGAAGATGTGAGCAAGAAATACAGTCACTTATCG 1740
 |||||
 Db 2190 CCTAGTGGCCCATCAAAACCTGAAGTGAAGATGTGAGCAAGAAATACAGTCACTTATCG 2249
 Oy 1741 TGGCAACCAAAATTTGAATTCAGAGCAACTCCAAATCTTATATTATAGAAAGCTTCAGC 1800
 |||||
 Db 2250 TGGCAACCAAAATTTGAATTCAGAGCAACTCCAAATCTTATATTATAGAAAGCTTCAGC 2309
 Oy 1801 CATGCATCTGTGTGAGCAGCTGGCAGACCGTGTGAGAGAAATGTGAAGACAGAAATCTGCC 1860
 |||||
 Db 2310 CATGCATCTGTGTGAGCAGCTGGCAGACCGTGTGAGAGAAATGTGAAGACAGAAATCTGCC 2369
 Oy 1861 ATTAAGAGACTCAAACTTAATGCAATTTACCTTCTCTGTGAGGGCAGCTAATGCAATAT 1920
 |||||
 Db 2370 ATTAAGAGACTCAAACTTAATGCAATTTACCTTCTCTGTGAGGGCAGCTAATGCAATAT 2429
 Oy 1921 GGAATTAAGTATCCAAAGCCAAATATCAGATCAGTGAAGAAACAGAAATGTCTTCCAAAC 1980
 |||||
 Db 2430 GGAATTAAGTATCCAAAGCCAAATATCAGATCAGTGAAGAAACAGAAATGTCTTCCAAAC 2489
 Oy 1981 AGTCAGGGGGGGGAGCAACAGCAGCAGTCCAGAGAGAGCTGGGAAATGCTGTTCTGACCTC 2040
 |||||
 Db 2490 AGTCAGGGGGGGGAGCAACAGCAGCAGTCCAGAGAGAGCTGGGAAATGCTGTTCTGACCTC 2549
 Oy 2041 CACAACCCCAACCGTCTCTTCTCTCTCTCCATCGAAGTGCAGTGGACAGTATGATCAACAG 2100
 |||||
 Db 2550 CACAACCCCAACCGTCTCTTCTCTCTCTCCATCGAAGTGCAGTGGACAGTATGATCAACAG 2609
 Oy 2101 TCTCAGTATATCAAGGATATAAATTTCTCTATGCGGCATCTGAGGCCAACCAGGGAGAA 2160
 |||||
 Db 2610 TCTCAGTATATCAAGGATATAAATTTCTCTATGCGGCATCTGAGGCCAACCAGGGAGAA 2669
 Oy 2161 TCAGACTGTGTAAGTTTTGAAGTGAAGCAGCCAGCCAAAAACAGTGTGATATCCCTGAT 2220
 |||||
 Db 2670 TCAGACTGTGTAAGTTTTGAAGTGAAGCAGCCAGCCAAAAACAGTGTGATATCCCTGAT 2279
 Oy 2221 CTCAGAAAGGGAGTCAACTATGAATTAAGCTGCGCCCTTTTATGAATTTCAAGGA 2280
 |||||
 Db 2730 CTCAGAAAGGGAGTCAACTATGAATTAAGCTGCGCCCTTTTATGAATTTCAAGGA 2789
 Oy 2281 GCAGATAGTGAATTCAGTGTGGCAAAACCTGGAAGAAAGACCCAGTGGCCCAACCCAA 2340
 |||||
 Db 2790 GCAGATAGTGAATTCAGTGTGGCAAAACCTGGAAGAAAGACCCAGTGGCCCAACCCAA 2849
 Oy 2341 GGTGTAATGTATCCAAAGATGGAAGAAAGAACTGCAATTTCTAGTATGTTGAGGAGCA 2400
 |||||
 Db 2850 GGTGTAATGTATCCAAAGATGGAAGAAAGAAAGAACTGCAATTTCTAGTATGTTGAGGAGCA 2909
 Oy 2401 CCTCCAGAGAGACTCAAAATGGAATGTGTCCAGAGATATAGGTTTGTGTCTGGGCAT 2460
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 Db 2910 CCTCCAGAGAGACTCAAAATGGAATGTGTCCAGAGATATAGGTTTGTGTCTGGGCAT 2969

Oy 2461 GAAACTCGATATACCACATCAACAAAACAGTGGATGGTTCACCTTTTCCGTGTCATTC 2520
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 Db 2970 GAAACTCGATATACCACATCAACAAAACAGTGGATGGTTCACCTTTTCCGTGTCATTC 3029
 Oy 2521 TTTCTTGTCTCGAATCCGATACAGTGTGAAGTGGACAGCAGTGGGCTGGGCT 2580
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 Db 3030 TTTCTTGTCTCGAATCCGATACAGTGTGAAGTGGACAGCAGTGGGCTGGGCT 3089
 Oy 2581 GGGGTAAAGAGTGAAGCTTCAGTTCATCCAGCTGGATGGCCATGGAACCTGTGACCT 2640
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 Db 3090 GGGGTAAAGAGTGAAGCTTCAGTTCATCCAGCTGGATGGCCATGGAACCTGTGACCT 3149
 Oy 2641 GAGGACCAAGTCAAGCTTCCTGCTGAGAGATTTCAATGATGTGTGAAGCAGCCGCTTCA 2700
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 Db 3150 GAGGACCAAGTCAAGCTTCCTGCTGAGAGATTTCAATGATGTGTGAAGCAGCCGCTTCA 3209
 Oy 2701 GCAGATATTGAGACAGCTGTGTGATCATCTTCATGCTTTCAGCATCTGCTTTATGCA 2760
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 Db 3210 GCAGATATTGAGACAGCTGTGTGATCATCTTCATGCTTTCAGCATCTGCTTTATGCA 3269
 Oy 2761 CACCGCAAGAGAAAGCGACTTACTAGTACTAGCGGGGTTCAGAAAAGTCCGCT 2820
 |||||
 Db 3270 CACCGCAAGAGAAAGCGACTTACTAGTACTAGCGGGGTTCAGAAAAGTCCGCT 3329
 Oy 2821 TTTACTTCAACCAACAGTAACTTACAGAGAGAGGCGAAGCTGTCAAGAGTGAAGG 2880
 |||||
 Db 3330 TTTACTTCAACCAACAGTAACTTACAGAGAGAGGCGAAGCTGTCAAGAGTGAAGG 3389
 Oy 2881 AGGCTGTGACTTTCACATCACTAGTGAAGCTGCGCCAGCAGCTGAGGAGACAGTGG 2940
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 Db 3390 AGGCTGTGACTTTCACATCACTAGTGAAGCTGCGCCAGCAGCTGAGGAGACAGTGG 3449
 Oy 2941 CCTAATCTGGCAACCAACCAATGAGTGTCTCATCAGCTGCTGCAAGGAGGCAATGGA 3000
 |||||
 Db 3450 CCTAATCTGGCAACCAACCAATGAGTGTCTCATCAGCTGCTGCAAGGAGGCAATGGA 3509
 Oy 3001 AACGAGCAGCAACCTCTACTACTACAGTGTGCGCCAGCTGATTTGATGAATTTAATAC 3060
 |||||
 Db 3510 AACGAGCAGCAACCTCTACTACTACAGTGTGCGCCAGCTGATTTGATGAATTTAATAC 3569
 Oy 3061 AACCACTGATTAACCAACCAACCAATGATGTCTGCTGATGATGATGATGATGAT 3120
 |||||
 Db 3570 AACCACTGATTAACCAACCAACCAATGATGTCTGCTGATGATGATGATGATGAT 3629
 Oy 3121 GTGACCTTGTATCAAAATCAATGAGATGAAACCTTCAATAGCCCAATTCGAGAT 3180
 |||||
 Db 3630 GTGACCTTGTATCAAAATCAATGAGATGAAACCTTCAATAGCCCAATTCGAGAT 3689
 Oy 3181 GGGGCTTTTGTCAATCAATCAAGGAGCTTACTCTTACGCGACCACTGAGCTGATCAG 3240
 |||||
 Db 3690 GGGGCTTTTGTCAATCAATCAAGGAGCTTACTCTTACGCGACCACTGAGCTGATCAG 3749
 Oy 3241 TCANAACCTACCAACCAATCAATGAGATGAAAGCTTCAATAGCCCAATTCGAGAT 3300
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 Db 3750 TCANAACCTACCAACCAATCAATGAGATGAAAGCTTCAATAGCCCAATTCGAGAT 3809
 Oy 3301 CCAGTGGAGCAGCAAGAAAGAAAGTGGCACAGTTCAGTCAACATCTGTGAGCAAAAC 3360
 |||||
 Db 3810 CCAGTGGAGCAGCAAGAAAGAAAGTGGCACAGTTCAGTCAACATCTGTGAGCAAAAC 3869
 Oy 3361 AAGCTGAACAAAGATTTATGAGCAATATGACACAGTTCCTCCAACTATGCCATACACCA 3420
 |||||
 Db 3870 AAGCTGAACAAAGATTTATGAGCAATATGACACAGTTCCTCCAACTATGCCATACCA 3929
 Oy 3421 TCATATGACCAAGACACAGAGAGATCCATCAACAGCTCAGACCGGGGAGATGATCATCT 3480
 |||||
 Db 3930 TCATATGACCAAGACACAGAGAGATCCATCAACAGCTCAGACCGGGGAGATGATCATCT 3989
 Oy 3481 GGGAGTCAAGGGGCAACAAAGGGGCAAGAACACCCCAAGTATCCCAAAACAGGTTGGCATG 3540
 |||||
 Db 3990 GGGAGTCAAGGGGCAACAAAGGGGCAAGAACACCCCAAGTATCCCAAAACAGGTTGGCATG 4049
 Oy 3541 AACTGGGCAAGACTGCTTCTCTCCGCCAGACATCTCTCTCAACAGCAATAGCCAA 3600

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Db 4050 AACTGGGCACACCTGCTCTCTCTCCCTCCCGACACATCTCTCTCCACACAGCAATAGGAA 4109
QY 3601 GAGTACACATTTCTGTAGTGAAGCTATGACCAGAAATGCCATGCTCCGTCACCA 3660
Db 4110 GAGTACACATTTCTGTAGTGAAGCTATGACCAGAAATGCCATGCTCCGTCACCA 4169
QY 3661 GCAGAGATGATTTGACACAGATGATTAAGAGAGAGAAAGATGAACAGAGGCCACT 3720
Db 4170 GCAGAGATGATTTGACACAGATGATTAAGAGAGAGAAAGATGAACAGAGGCCACT 4229
QY 3721 CCCCCTGTTGCGGAGAGAGCTTCTTCCAGCTGCCGTGCTATATACCATAGTCCACT 3780
Db 4230 CCCCCTGTTGCGGAGAGAGCTTCTTCCAGCTGCCGTGCTATATACCATAGTCCACT 4289
QY 3781 GCCACTGTGACTCCCTCCACAGAAATCCAGCCCATGTTACAGATTTGTCCAGAG 3840
Db 4290 GCCACTGTGACTCCCTCCACAGAAATCCAGCCCATGTTACAGATTTGTCCAGAG 4349
QY 3841 GAGACTGGCCACATGACACAGCCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3900
Db 4350 GAGACTGGCCACATGACACAGCCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4409
QY 3901 CCACACAGGCGGATCTCTCCCTCCACATACCTATGCTATATTCAGAGACCCCTGCTCA 3960
Db 4410 CCACACAGGCGGATCTCTCCCTCCACATACCTATGCTATATTCAGAGACCCCTGCTCA 4469
QY 3961 GATATGATACGGATGCGCCAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 4020
Db 4470 GATATGATACGGATGCGCCAGAAAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 4529
QY 4021 ATGCAAAACGAAAGGCTTTGTTACGTGGCTTGAGCAGACACCTGCTCAGGTGGG 4080
Db 4530 ATGCAAAACGAAAGGCTTTGTTACGTGGCTTGAGCAGACACCTGCTCAGGTGGG 4589
QY 4081 GACCTGAGAGACTCTGTCACAGGGGTCATATCAACGGCTGGGGCTTCAGCCTCAGAGAG 4140
Db 4590 GACCTGAGAGACTCTGTCACAGGGGTCATATCAACGGCTGGGGCTTCAGCCTCAGAGAG 4649
QY 4141 GACAACATTTCCAGCGAGCCTCCAGTGTATGTTCTTCGAGCGGCTCTTTTCTACTGAT 4200
Db 4650 GACAACATTTCCAGCGAGCCTCCAGTGTATGTTCTTCGAGCGGCTCTTTTCTACTGAT 4709
QY 4201 GCTGACTTTGCCAGGAGTGCAGAGCAGCGGAGAGATCTGTGTAAGTATGACAGA 4260
Db 4710 GCTGACTTTGCCAGGAGTGCAGAGCAGCGGAGAGATCTGTGTAAGTATGACAGA 4769
QY 4261 CGGCAAAATGACAGATGCTGCTGCGCTGCATTTTCATGCTCAGTGCCTAGGCC 4320
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QY 4321 ACAAGTCCGCTGTCTACAGACAGACATAGATGCGCGCTAATGCAAAACAGAGCA 4380
Db 4830 ACAAGTCCGCTGTCTACAGACAGACATAGATGCGCGCTAATGCAAAACAGAGCA 4889
QY 4381 GCCAAGAACTGAACACAGCCAGGACATCTGCGAGAGAACTACACAGATGATCTT 4440
Db 4890 GCCAAGAACTGAACACAGCCAGGACATCTGCGAGAGAACTACACAGATGATCTT 4949
QY 4441 CCACACACTCTGCTGCCGACCTGCTATTAAGTACACTTACTGCCAATCCAAAGACAG 4500
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QY 4501 CTGGAAGTACAGCTGTAGTGTGCGCAAACTCCCTCTATGGATGCAAGACAGACAGA 4560
Db 5010 CTGGAAGTACAGCTGTAGTGTGCGCAAACTCCCTCTATGGATGCAAGACAGACAGA 5069
QY 4561 TCATCAGACAGAAAGAGACAGTATACAGGGAGAGAGAGAGAGAGAGAGAGAGAGTT 4620
Db 5070 TCATCAGACAGAAAGAGACAGTATACAGGGAGAGAGAGAGAGAGAGAGAGAGTT 5129
QY 4621 GTTGACATGGCAAAATCCAGGTGATCCAGAGAGACACAGAGACAGCAAAATGACGGG 4680

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Db 5130 GTTGACATGGCAAAATCCAGGTGATCCAGAGAAACAGACAGAGAGAGAGAGAGAG 5189
QY 4681 AAAGAGCTGGAACAAAGAGCAAAAGACCTTCCACAGCAAAAGACTCATCTCATC 4740
Db 5190 AAAGAGCTGGAACAAAGAGCAAAAGACCTTCCACAGCAAAAGACTCATCTCATC 5249
QY 4741 CAAGAGATATTTCTACTTATTTGAGACCTACTTTTCCAAACATCAAAATATCCAGAGAT 4800
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QY 4801 CCAAGTCTCTCAAGCTCAATGTCATCAAGAGAGATCAGAGAGAGAGAGAGAGAGAGAG 4856
Db 5310 CCAAGTCTCTCAAGCTCAATGTCATCAAGAGAGATCAGAGAGAGAGAGAGAGAGAGAG 5365

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Search completed: September 20, 2002, 12:00:25
 Job time: 39 sec

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